MINAR International Journal of Applied Sciences and Technology
ISSN: 2717-8234
Article type: Research Article

Received: 15/05/2022 **Accepted:**10/06/2022 **Published:** 01/09/2022

SEPARATION AND IDENTIFICATION OF A NUMBER OF UNSATURATED FATTY ACIDS FROM DIFFERENT TYPES OF ALGAE

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Abstract:

Seven cotton genotypes were grown in a different environmental conditions (as a combination among plant densities: 15, 20, and 25 cm under salt and non salt stress irrigation) to estimate genetic behavior in different environments of cotton genotypes (Ceebro, W888, Pac-cot189, Lashata, Cocker310, Montana, and Ik259).Analysis of variance for the interaction environments with the genotypes according to Randomized Completely Block Design with three replications were used, furthermore GGE biplot analysis for the seed cotton yield. Results Showed: Environments affected high significant in seed cotton yield for studied genotypes. Genotypic and genotypic environmental interaction contribute of 14.7 and 32.2% of variation respectively. PC1 and PC2 interpreted 53.9 and 26.5 % respectively of differences in GGE variances.IK259 Genotype the most productive and stable than others for high PC1 and low absolute value of PC2.E6 environment correlated significant and positive with other environments that means the effect of salt water stress in a wide distance among plants (25cm). Better performance of IK259 genotype was under un salt stress conditions in narrow distances among plants(15 cm). While Pac-cot genotype was favorable in most salt stress conditions. Consequently IK259 and Pac-cot189 genotypes are productive and desirable in studied environments.

Keywords: Cotton Genotypes, Environments, GGE Bi-Plot Analysis.

http://dx.doi.org/10.47832/2717-8234.12.38

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Introduction:

The important of cotton fiber crops came out from their superior quality characteristics of lint cotton to the other natural fibers. Quantity lint yield controlled by the genetic ability which may be interpreted by environments factors. Recent years showed deterioration of seed cotton yield though existence many cultivars in Iraq, which can be justification by the shortage information about performance and stability of genotypes across wide range of environments. Potential yield can be consist by the genetic ability which can be drift by environmental factors. Therefore, stability approaches are important idea in understand behavior trait in environment or multi traits in multi environments [1] Each plant breeding program should be involve understanding the stability of yield across wide range of environments that regard the final step for promising genotype before recommend of depend the preferable genotype in a relevant environments. Many statistical and genetical approaches proposed from plant breeder such as Finally and Wilkinson 1963 , Ebrhart and Rusell, 1966 Shukula and GGE biplot methods [2,3]. GGE biplot method is the most graphical modern method technique in distinguish genotype performance in multi environments [4]. High performance of genotype under different environmental conditions is a most important goal in breeding program, therefore the interaction must be consider through testing potential ability under different environmental conditions [5]. GGE biplot analysis use principal component analysis in explanations the differences among genotypes in terms of figures illustrate variability caused differences in traits in terms of stability parameters [6,7]. Seed cotton yield and it's components almost aren't congruent in their performance in different environments [8,9]. Stable genotype doesn't affect by changing environments and in a high delimited and breeding value of breeding program [10].GGE bi-plot explain relationships among genotypes, and environments in addition of interactions, better genotypes for each environments and ideal genotype according to their direction ability and variability in principle component analysis. The study aimed to determine ability and stability for seed cotton yield under different environment of cotton genotypes.

Materials and Methods

A study performed at agriculture field crops farm\ Baghdad governorate\ Al-Mahmoodiyah district(33.05N latitude, 44.32E longitude) to estimate genotypic environmental interaction by using GGE bi-plot analysis for seven cotton genotypes(table 1).

Table . 1 Genotypes Names and sources

No.	Symbol	Genotype	Origin
1	G1	Ceebro	Greece
2	G2	W888	USA
3	G3	Pac-Cot 189	USA
4	G4	Lashata	Espain
5	G5	Cocker 310	USA
6	G6	Montana	USA
7	G7	IK259	Greece

Environmental treatments obtained from combinations among plant distances:15, 20 and 25 cm and salt stress irrigation: 1 and 6 $d.m^{-1}$, resulted in six environments(E1:15 cm*1 $d.m^{-1}$, E2:15cm*6 $d.m^{-1}$, E3:20cm*1 $d.m^{-1}$, E4:20cm*6 $d.m^{-1}$, E5:25cm*1 $d.m^{-1}$, E6:25cm*6 $d.m^{-1}$).Seeds grown in 20/ 4/ 2020 after estimation soil chemical properties as shown in table

2.Two types of irrigation water was used: River irrigation water (EC=1 $d.m^{-1}$) and salt irrigation water (6 $d.m^{-1}$ obtained from adding salt to water till reach determined regime).

Table 2. Soil properties

No.	Characteristics	Rank	Unit
1	Ph	7.7	
2	Organic matter	15.5	$gram.kilogram^{-1}$
3	N	10	$Milligram.Kilogram^{-1}$
4	P	15.1	$Milligram.Kilogram^{-1}$
5	K	54.5	$Milligram.Kilogram^{-1}$
6	Na	93.3	$Milligram.Kilogram^{-1}$
7	Sand	501	$gram.kilogram^{-1}$
8	Silt	263	$gram.kilogram^{-1}$
9	Clay	224	$gram.kilogram^{-1}$
10	Texture	Sandy Clay Loam	
11	Un Salt stress treatments EC	6.3	
12	Salt Stress treatment Ec	9.7	

GGE bi-plot analysis performed for significant interactions of genotypes with environments only. Statistical analysis focus on two concepts: genotype and genotype environment are used to evaluate genotypes and depend on multi environment yield trails by using PC1 and PC2.According to [1] single value partitioned in two components: Y_{ij}- μ-$\beta_{j=}$ $\lambda 1 \varepsilon i1$ $\eta j1+\lambda 2$ $\varepsilon i2 \eta j2+Eij...1.$ Y_{ij}:performance i genotype in j environment , μ:average mean , ʎ1 and ʎ2: SDV for the two components PC1 and PC2 respectively , βj: main effect of environment, $\varepsilon i1$, $\varepsilon i2$: eigenvector of the two principle components of I genotype, $\eta j1$, $\eta j2$: eigenvectors for the two principle components of j environment, Eij: standered error for i'th genotype in j;th environment. G_{i1} = ʎ1 $^{fi}\varepsilon i1$, $e_{1j=}$ ʎ1 1^{1-f} $\eta j1....2,$ fi: fraction coefficient for PC1 values . Calculating GGE bi-plot through following equation: Y_{ij}- μ-$\beta_{j=}$ gi1 e1j +gi2 e2j +Eij …3 , and the adjusted data the equation will be: Y_{ij}- μ-$\beta_j/s_{j=}$ $\sum_I{}^k g_{i1} e_{1j}$ + Eij…4 S_j: standered divation in j environment , i=1…k, gi1 and e1j are PC1 values for I genotype in j environment. Third and forth equation were used in calculating relationships among genotypes and environments and other concepts of GGE bi-plot analysis. [11].

Results and Discussion

Analysis of variance performed in each environment alone to estimate pooled deviation which used in testing significant genotypic environmental interactions. Significant interactions appear in seed cotton yield (table 3) outcome from variability trait behavior and direction response in different environments which evidence genetic variability among genotypes even though from different origin places.

Table 3. Pooled analysis of Seed cotton yield

Environments	S.O.V.	df	MS
E1	Replicates	6	1542551.70**
	Genotypes	12	3902300.85**
	Experimental error	2	203442.04
E1	Replicates	6	442699.11ns
	Genotypes	12	1009177.17*
	Experimental error	2	274238.91
E3	Replicates	6	739716.52ns
	Genotypes	12	1842491.90**
	Experimental error	2	221226.51
E4	Replicates	6	861888.79**
	Genotypes	12	388481.22*
	Experimental error	2	120682.05
E5	Replicates	6	1359570.37*
	Genotypes	12	1018028.98*
	Experimental error	2	282089.38
E6	Replicates	6	508869.05*
	Genotypes	12	410120.18*
	Experimental error	2	129909.59
Pooled analysis	environments	5	34832966.46**
	Genotypes	6	8081922.50ns
	Interaction	30	3525976**

SS portion,53.02 ,14.76 , 32.2 % for environment, genotype and interaction respectively

Accordingly GGE bi-plot analysis achieved to interpret the relationships among genotypes and environments via PC1 and PC2 estimate in different concepts of out puts (Mare et al , 2020). Most variability were in PC1 (53.9%) followed by 26.5% in PC2 and both principle analysis explained 80.4% of differences in GGE bi-plot analysis. Genotypes that have PC1 higher than zero classified as high yielded and vice-versa for the other genotypes possessed below zero PC1 values. Other than the magnitude absolute value of PC2 refer to unstable while genotypes points closest to PC2 zero axis are stable in their trait. Genotypes divided in three categories: first were high yield and stable (G7) which PC1 higher than 1 and low absolute value of PC2. Second category (G3 and G5) possessed high yield though unstable performance. Third group involve G1,G2,G4 and G6 have low yield though many of them near zero axis (fig.1).

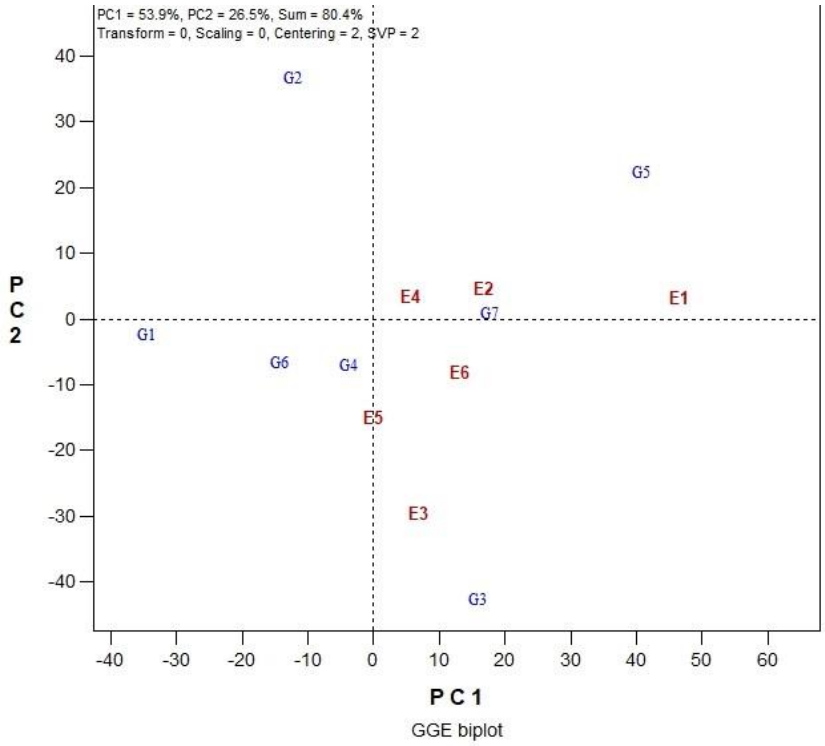

Fig.1:Relation among genotypes and environments

Statistical concepts can be understood as a similarity environments and relationships among environments can be presented in fig.2. Whole environments are positive values in PC1 except E5 which means the similarity of genotypes responses in most studied environments and selection can be applied by same manner in multiple environments [12]. Straight line from the origin point to the environment value represent standard deviation of environment. While analogous cosine angle between two environmental vectors and any increases in standard deviation lead to increasing environmental ability in classification genotypes [2]. Most angles are less than 90 degree except E4 and E5 that agree with the correlation results in table (4).

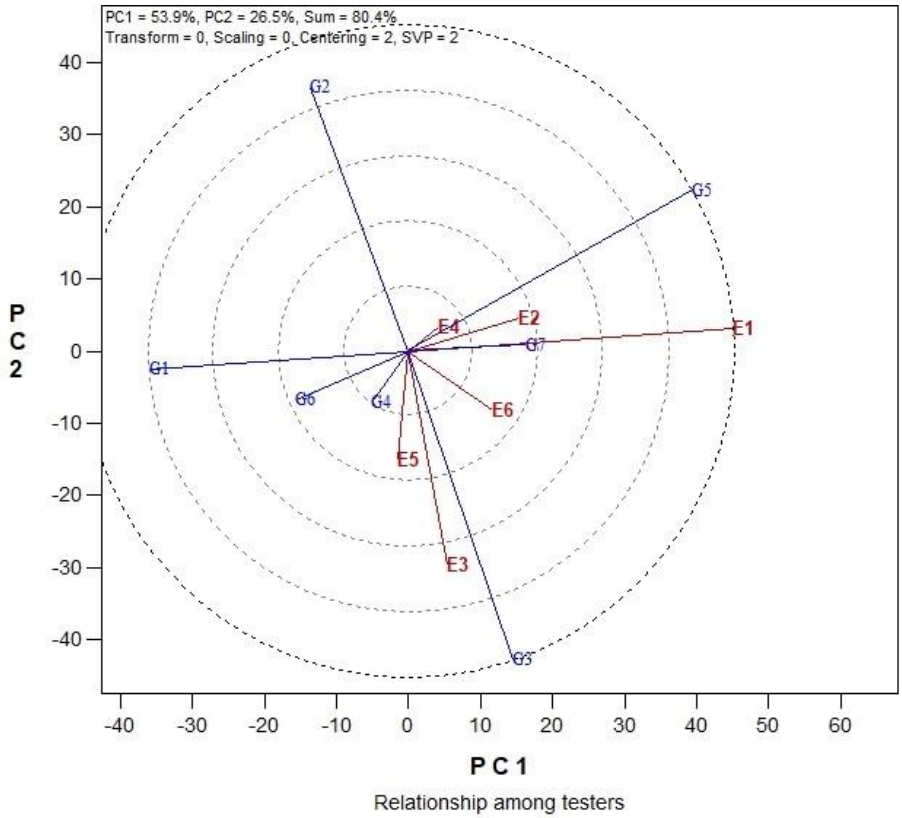

Fig.2: relation among environments

Non significant correlations among E4 and E5 environments and differ from each other in their effects in studied genotypes while significant positive correlations appear among other environments. Absence negative correlation refer to the similar performance of genotypes in different environments and removal of one of pair correlated environments aren't affect on the other environment [13,14]. E1 is the best environment for their high PC1 and low obsolut PC2 value.

Table 4.correlation coefficients among environments

	E1	E2	E3	E4	E5	E6
E6	0.9*	0.91*	0.89*	0.87*	0.86*	1
E5	0.62ns	0.8ns	0.81ns	0.74ns	1	
E4	0.81ns	0.85*	0.75ns	1		
E3	0.69ns	0.73ns	1			
E2	0.87*	1				
E1	1					

Genotypes performance in a favorable environments can be shown in a polygon shape drawn by straight line connection among farest genotypes points from origin point which involve whole other genotypes(fig,4). High yield obtained from G5 and G7 in E1,E2 and E4 environments, other than G4 and G3 have better performance in E3,E5 and E6 environments. Remarkable favorite environment characteristics that their ability in classified genotypes according to high PC1 and Low absolute PC2 values (Yan et al, 2001). Two mega-environments appear in Fig.4: first (E1,E2 and E4) and second (E3,E5 and E6). The best performance of

genotype in favorable environment is the most important goal of plant breeder [10]. Therefore, G4 was high productive in the first mega environments followed by G3 in the second mega environments.

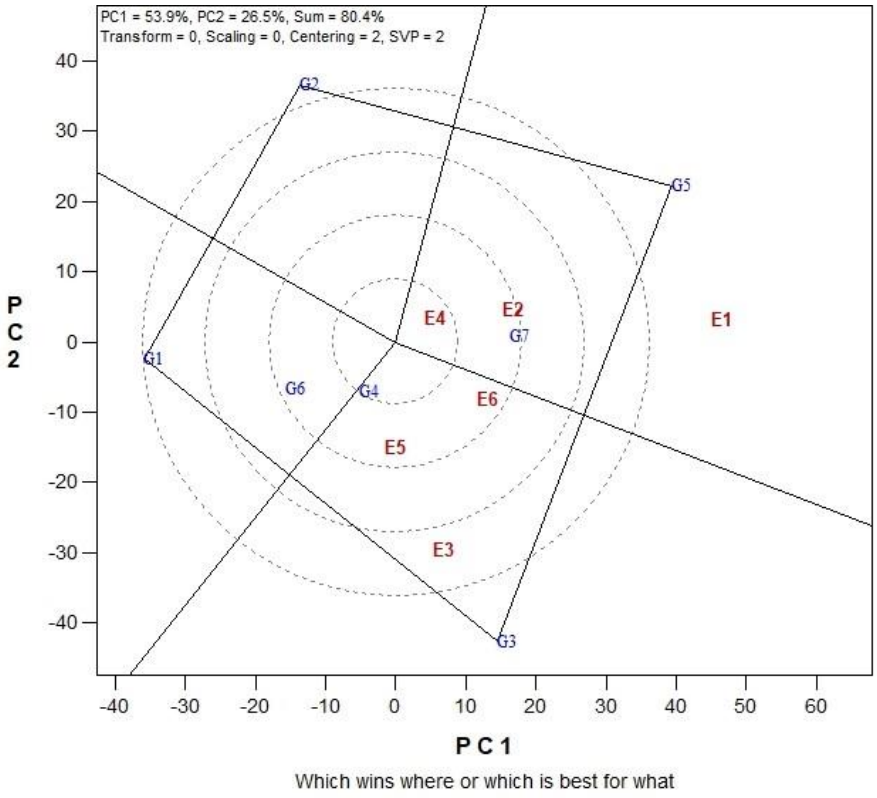

Fig.3: favorable genotypes in environments

Stability genotypes can be predicted by drawing two axis: x-represent AEC (Average Environment Coordination) and determined by average PC1 and PC2 of whole environments. While the second axis drawn vertically on the first axis and both axis passing through original point. AEC axis classified genotypes in two groups: first lay on the right direction which high yield (up to average yield) (G3,G5 and G7) and second include low yield group on the other direction(G1,G2,G4 and G6). Other than Y-axis refer to stability of genotypes according to their distance from average line (Hamadalla et al ,2011). Shortest vectors are more stable than others [10,15]. Consequently G7 genotype was more productive and stable in seed cotton yield per hectare (Fig.4).

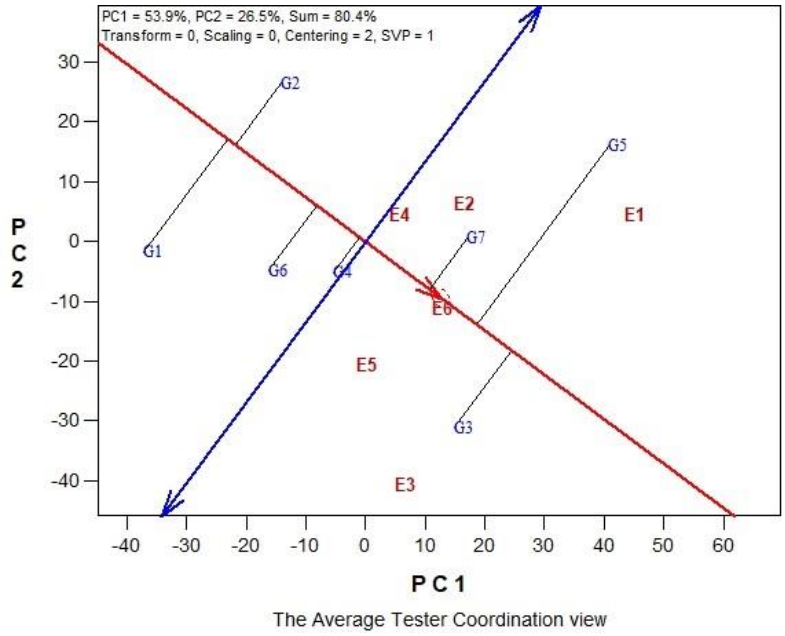

Fig.4: stability genotypes

The other of GGE bi-plot analysis is the similarity and differences of genotypes behavior in the same environment or multi environment in consequences of their performance from general mean. The differences represents as victors from original point to the genotype value (distances from general mean). Vectors of G3 and G5 are the tallest and best performance in yield per unit area to the other genotypes. G1 is the lesser in yield and worse in one or multi environments(Fig.5). Cosine angle between both two genotypes refer to similarity and vice versa[16]. Small angle between G5 and G3 vectors diminished differences in response to the genotypic environmental interaction compare with G1. Genotypes near origin point (G4,G6 and G7) have yield close to the average, though similarity or un similarity among them.

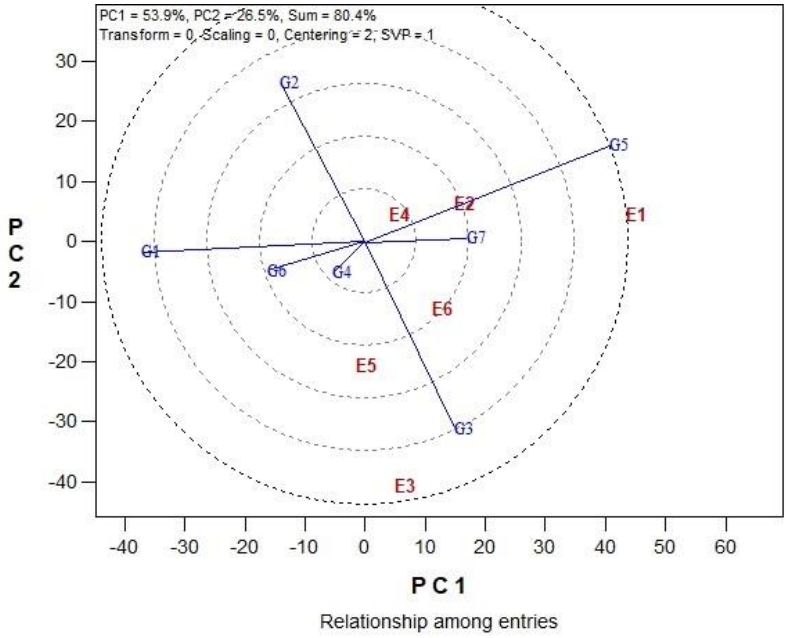

Fig.5: relation among entries

Estimation typical genotype in Fig.6 depend on two essential concepts: High yield and stable performance in different environments . By the same manner typical genotype has low deviation from it's average yield and from over all mean in different environments and keep it's production steady across multi environments besides neglected of genotypic environmental interaction [15]. Typical genotype posses longest vector to the other genotypes and focus on the central circle which determined the best production and stable genotype.(Fig.6) Showed that G7 is the nearest to the central circle followed by G3 that considered promising genotype in production stable seed cotton yield per unit area. While G1 is the farest and worst in seed cotton yield as a result of farest from circle of typical genotype.

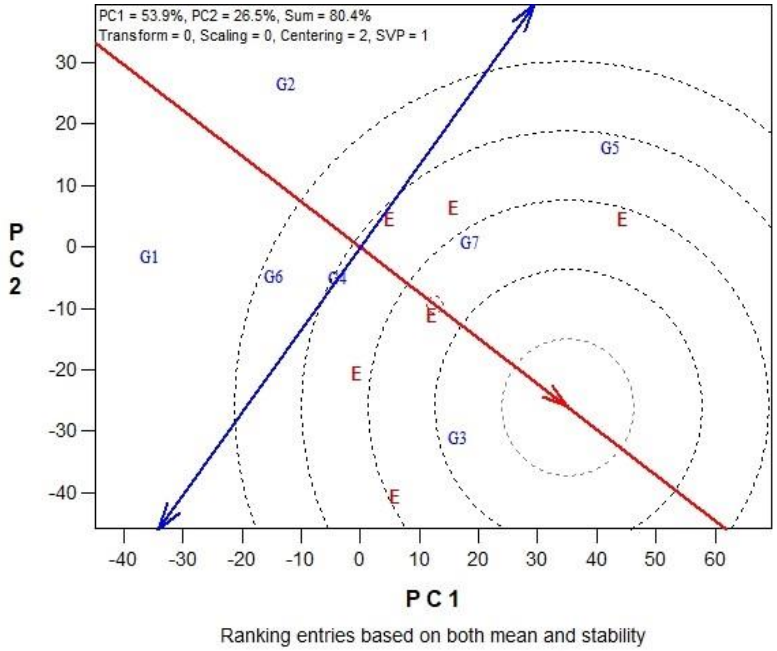

Fig.6: Ideal genotype

Conclusion

G7 can be considered as productive and stable genotype under un stress conditions (E2 and E4) followed by G3 in the second mega environments (stress conditions: E5 and E6).

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